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Figure 1. Sequence of *C. pneumoniae* ATP-binding cassette gene

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acttcccccc tgctaaacta tgctcagata atgctgctat gattgcaggt ctagggggag 60

aaaattttca aaaaaactct agtattccgg aaattcgtat atg cgc aag ata tca 115
                                     Met Arg Lys Ile Ser
                                     1         5

gtg gga atc tgt atc acc att ctc ctt agc ctc tcc gta gtc ctc caa 163
Val Gly Ile Cys Ile Thr Ile Leu Leu Ser Leu Ser Val Val Leu Gln
                                     10         15         20

ggc tgc aag gag tcc agt cac tcc tct aca tct cgg gga gaa ctc gct 211
Gly Cys Lys Glu Ser Ser His Ser Ser Thr Ser Arg Gly Glu Leu Ala
                                     25         30         35

att aat ata aga gat gaa ccc cgt tct tta gat cca aga caa gtg cga 259
Ile Asn Ile Arg Asp Glu Pro Arg Ser Leu Asp Pro Arg Gln Val Arg
                                     40         45         50

ctt ctt tca gaa atc agc ctt gtc aaa cat atc tat gag gga tta gtt 307
Leu Leu Ser Glu Ile Ser Leu Val Lys His Ile Tyr Glu Gly Leu Val
                                     55         60         65

caa gaa aat aat ctt tca gga aat ata gag cct gct ctt gca gaa gac 355
Gln Glu Asn Asn Leu Ser Gly Asn Ile Glu Pro Ala Leu Ala Glu Asp
                                     70         75         80         85

tac tct ctt tcc tcg gac gga ctc act tat act ttt aaa ctg aaa tca 403
Tyr Ser Leu Ser Ser Asp Gly Leu Thr Tyr Thr Phe Lys Leu Lys Ser
                                     90         95         100

gct ttt tgg agt aat ggc gac ccc tta aca gct gaa gac ttt ata gaa 451
Ala Phe Trp Ser Asn Gly Asp Pro Leu Thr Ala Glu Asp Phe Ile Glu
                                     105         110         115

tct tgg aaa caa gta gct act caa gaa gtc tca gga atc tat gct ttt 499
Ser Trp Lys Gln Val Ala Thr Gln Glu Val Ser Gly Ile Tyr Ala Phe
                                     120         125         130

gcc ttg aat cca att aaa aat gta cga aag atc caa gag gga cac ctc 547
Ala Leu Asn Pro Ile Lys Asn Val Arg Lys Ile Gln Glu Gly His Leu
                                     135         140         145

tcc ata gac cat ttt gga gtg cac tct cct aat gaa tct aca ctt gtt 595
Ser Ile Asp His Phe Gly Val His Ser Pro Asn Glu Ser Thr Leu Val
                                     150         155         160         165

gtt acc ctg gaa tcc cca acc tcg cat ttc tta aaa ctt tta gct ctt 643
Val Thr Leu Glu Ser Pro Thr Ser His Phe Leu Lys Leu Leu Ala Leu
                                     170         175         180

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Sequence 294360

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Figure 1 Cont.

cca gtc ttt ttc ccc gtt cat aaa tct caa aga acc ctg caa tcc aaa	691
Pro Val Phe Phe Pro Val His Lys Ser Gln Arg Thr Leu Gln Ser Lys	
185 190 195	
tct cta cct ata gca agc gga gct ttc tat cct aaa aat atc aaa caa	739
Ser Leu Pro Ile Ala Ser Gly Ala Phe Tyr Pro Lys Asn Ile Lys Gln	
200 205 210	
aaa caa tgg ata aaa ctc tca aaa aac cct cac tac tat aat caa agt	787
Lys Gln Trp Ile Lys Leu Ser Lys Asn Pro His Tyr Tyr Asn Gln Ser	
215 220 225	
cag gtg gaa act aaa acg att acg att cac ttc att ccc gat gca aac	835
Gln Val Glu Thr Lys Thr Ile Thr Ile His Phe Ile Pro Asp Ala Asn	
230 235 240 245	
aca gca gca aaa cta ttt aat cag gga aaa ctc aat tgg caa gga cct	883
Thr Ala Ala Lys Leu Phe Asn Gln Gly Lys Leu Asn Trp Gln Gly Pro	
250 255 260	
cct tgg gga gaa cgc att cct caa gaa acc cta tcc aat tta cag tct	931
Pro Trp Gly Glu Arg Ile Pro Gln Glu Thr Leu Ser Asn Leu Gln Ser	
265 270 275	
aag ggg cac tta cac tct ttt gat gtc gca gga acc tca tgg ctc acc	979
Lys Gly His Leu His Ser Phe Asp Val Ala Gly Thr Ser Trp Leu Thr	
280 285 290	
ttc aat atc aat aaa ttc ccc ctc aac aat atg aag ctt aga gaa gcc	1027
Phe Asn Ile Asn Lys Phe Pro Leu Asn Asn Met Lys Leu Arg Glu Ala	
295 300 305	
tta gca tca gcc tta gat aag gaa gct ctt gtc tca act ata ttc tta	1075
Leu Ala Ser Ala Leu Asp Lys Glu Ala Leu Val Ser Thr Ile Phe Leu	
310 315 320 325	
ggc cgt gca aaa act gcc gat cat ctc cta cct aca aat att cat agc	1123
Gly Arg Ala Lys Thr Ala Asp His Leu Leu Pro Thr Asn Ile His Ser	
330 335 340	
tat ccc gaa cat caa aaa caa gag atg gca caa cgc caa gct tac gct	1171
Tyr Pro Glu His Gln Lys Gln Glu Met Ala Gln Arg Gln Ala Tyr Ala	
345 350 355	
aaa aaa ctc ttt aaa gaa gct tta gaa gaa ctc caa atc act gct aaa	1219
Lys Lys Leu Phe Lys Glu Ala Leu Glu Glu Leu Gln Ile Thr Ala Lys	
360 365 370	
gat ctc gaa cat ctt aat ctt atc ttt ccc gtt tcc tcg tca gca agt	1267
Asp Leu Glu His Leu Asn Leu Ile Phe Pro Val Ser Ser Ser Ala Ser	
375 380 385	

Sequence 1

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Figure 2. Restriction enzyme analysis of the *C. pneumoniae*
ATP-binding cassette gene

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                                BseMII  CviRI
                                BspMI|  HaeIV
                                DdeI |  Fnu4HI ||  Hin4I
                                BbvI | |  TseI || |  MwoI |  BfaI
                                | | |  || | |  | |
ACTTCCCCCTGCTAAACTATGCTCAGATAATGCTGCTATGATTGCAGGTCTAGGGGGAG
1  -----+-----+-----+-----+-----+-----+ 60
TGAAGGGGGGACGATTTGATACGAGTCTATTACGACGATACTAACGTCCAGATCCCCCTC

                                ApoI
                                Tsp509I
                                Hpy178III |
                                XmnI      MspI |
                                ApoI |      BsaWI |      HinfI
Tsp509I |      BfaI  Kpn2I |      HhaI      TfiI
                                | |      | |      FspI| EcoRV  TspRI
                                | |      | |      | |      |
AAAATTTTCAAAAAAATCTAGTATTCGGAAATTCGTATATGCGCAAGATATCAGTGGG
61 -----+-----+-----+-----+-----+-----+ 120
TTTTAAAAGTTTTTTTGAGATCATAAGGCCTTTAAGCATATACGCGTTCTATAGTCACCC

                                CviRI      MaeIII
                                MnlI|      Tsp45I
                                Fnu4HI||      BspGI |
                                CviJI      BsaJI || |      BsrI |
                                Bpu10I |      MnlI |CviJI|||      BseRI | |
HphI      DdeI |      BbvI | StyI TseI|||HinfI | | |
                                | |      | |      | | | | |
AATCTGTATCACCATTCTCCTTAGCCTCTCCGTAGTCCTCCAAGGCTGCAAGGAGTCCAG
121 -----+-----+-----+-----+-----+-----+ 180
TTAGACATAGTGGAAGAGGAATCGGAGAGGCATCAGGAGGTTCCGACGTTCTCCTCAGGTC

                                Sth132I
                                AlwI |
                                Sth132I  MnlI      MseI      CjeI |
PleI      |      Aval|      VspI      BscGI | |
                                | |      | |      | |
TCACTCCTCTACATCTCGGGGAGAACTCGCTATTAATATAAGAGATGAACCCCGTTCTTT
181 -----+-----+-----+-----+-----+-----+ 240
AGTGAGGAGATGTAGAGCCCCTCTTGAGCGATAATTATATTCTCTACTTGGGGCAAGAAA

                                DpnI
                                BstYI |
                                Sau3AI |
                                | |
                                CjeI
                                Hpy188IX | CviJI      MslI
                                | |      | |      MnlI |Tth111III
AGATCCAAGACAAGTGC GACTTCTTT CAGAAATCAGCCTTGTC AAACATATCTATGAGGG
241 -----+-----+-----+-----+-----+-----+ 300
TCTAGGTTCTGTT CACGCTGAAGAAAGCTTTAGTCGGAACAGTTTGTATAGATACTCCC

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Figure 2 Cont.

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                                Cac8I
Hpy178III   Hpy178III   CviJI |   CviRI   BbsI
|           |           |   |           |
ATTAGTTCAAGAAAATAATCTTTCAGGAAATATAGAGCCTGCTCTTGCAGAAGACTACTC
301 -----+-----+-----+-----+-----+-----+-----+ 360
TAATCAAGTTCTTTTATTAGAAAGTCCTTTATATCTCGGACGAGAACGTCTTCTGATGAG

Hpy188IX
PleI|
BsaJI | | MnlI   DraI   AluI
MboII | | HinfI|   MseI|   CviJI
|   |   |   |   |   |
TCTTTCCTCGGACGGACTCACTTATACTTTTAACTGAAATCAGCTTTTTGGAGTAATGG
361 -----+-----+-----+-----+-----+-----+-----+ 420
AGAAAGGAGCCTGCCTGAGTGAATATGAAAATTTGACTTTAGTCGAAAACCTCATTACC

AluI   Hpy178III
CviJI   SmlI |
MspAII   MboII Bce83I   AluI | |
SimI   MseI PvuII   BbsI TfiI Eco57I   CviJI | |
|   |   |   |   |   |   |   |
CGACCCCTTAACAGCTGAAGACTTTATAGAATCTTGAAACAAGTAGCTACTCAAGAAGT
421 -----+-----+-----+-----+-----+-----+-----+ 480
GCTGGGAATTGTCGACTTCTGAAATATCTTAGAACCTTTGTTTCATCGATGAGTTCTTCA

DpnI
HinfI   MnlI|
TfiI   BstYI||
BsmAI |   Tsp509I |   Sau3AI||
Hpy178III| |   HinfI | |   AlwI | | |
DdeI | | |   BseMII   TfiI | |   RsaI| | |
| | |   |   |   |   |   |   |
CTCAGGAATCTATGCTTTTGCCTTGAATCCAATTAATAAATGTACGAAAGATCCAAGAGGG
481 -----+-----+-----+-----+-----+-----+-----+ 540
GAGTCCTTAGATACGAAAACGGAAGTTAGGTTAATTTTACATGCTTTCTAGGTTCTCCC

BseSI
BsiHKA I
Bsp1286I
CviRI |   BsaJI
MnlI   MjaIV |   HinfI   EcoRII
BsmFI |   ApaLI | |   TfiI   MaeIII |
|   |   |   |   |   |   |
ACACCTCTCCATAGACCATTTTGGAGTGCCTCTCCTAATGAATCTACACTTGTTGTTAC
541 -----+-----+-----+-----+-----+-----+-----+ 600
TGTGGAGAGGTATCTGGTAAAACCTCACGTGAGAGGATTACTTAGATGTGAACAACAATG

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Figure 2 Cont.

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                                AluI
                                CviJI
                                EarI
HinfI      TfiI      MseI      CjePI      SapI
ScrFI      |      MnlI      MboII      |      BsrI      BscGI
|      |      |      |      |      |
CCTGGAATCCCCAACCTCGCATTTCTTAAACTTTTAGCTCTTCCAGTCTTTTTTCCCGT
601 -----+-----+-----+-----+-----+-----+ 660
GGACCTTAGGGGTTGGAGCGTAAAGAATTTTGAAAATCGAGAAGGTGAGAAAAGGGGCA

                                AluI
                                CviJI
                                MwoI
                                AcI      |      |
Sth132I CjePI      CviRI      SfcI      Cac8I      |      |
|      |      |      |      |      |      |
TCATAAATCTCAAAGAACCTGCAATCCAAATCTCTACCTATAGCAAGCGGAGCTTTCTA
661 -----+-----+-----+-----+-----+-----+ 720
AGTATTTAGAGTTTCTTGGGACGTTAGGTTTAGAGATGGATATCGTTTCGCCTCGAAAGAT

                                Tth111II
                                MnlI
TCCTAAAAATATCAAACAAAAACAATGGATAAACTCTCAAAAAACCCTCACTACTATAA
721 -----+-----+-----+-----+-----+-----+ 780
AGGATTTTTATAGTTTGTGTTTGTACCTATTTTGAGAGTTTTTTGGGAGTGATGATATT

                                Sth132I      Fnu4HI
                                HinfI      Hpy178III      TseI
                                TfiI      SfaNI      |      CviRI      MwoI      |
                                |      |      |      |      |      |
TCAAAGTCAGGTGGAAACTAAACGATTACGATTCACTTCATTCCCAGTCAAACACAGC
781 -----+-----+-----+-----+-----+-----+ 840
AGTTTCAGTCCACCTTTGATTTTGCTAATGCTAAGTGAAGTAAGGGCTACGTTTGTGTCTG

                                AvaII      MnlI
                                EcoO109I      Bce83I
                                Psp5II      BslI
                                MseI      BbvI      MunI      Sau96I      BsaJI      |      BsmI
Tth111III      |      Tsp509I      Sse8647I      StyI      |      |      XmnI
|      |      |      |      |      |      |      |
AGCAAACTATTTAATCAGGGAAAACCTCAATTGGCAAGGACCTCCTTGGGGAGAACGCAT
841 -----+-----+-----+-----+-----+-----+ 900
TCGTTTTGATAAATTAGTCCCTTTTGAGTTAACCGTTCCTGGAGGAACCCCTCTTGCGTA

                                BseSI
                                Hpy178III      Tsp509I      DdeI      Bsp1286I
                                SmlI      |      MnlI      |      Bst4CI      |      BmgI
                                |      |      |      |      |      |
TCCTCAAGAAACCCTATCCAATTTACAGTCTAAGGGGCACTTACACTCTTTTGATGTGCG
901 -----+-----+-----+-----+-----+-----+ 960
AGGAGTTCTTTGGGATAGGTTAAATGTCAGATTCCTCGTGAATGTGAGAAAACCTACAGCG

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MnlI
 CviJI
 NlaIII
 HphI
 NlaIV
 ApoI
 Tsp509I
 DdeI
 AluI
 CviJI
 HindIII
 MnlI
 AGGAACCTCATGGCTCACCTTCAATATCAATAAATTCCCCCTCAACAATATGAAGCTTAG
 961 -----+-----+-----+-----+-----+-----+-----+ 1020
 TCCTTGGAGTACCGAGTGAAGTTATAGTTATTTAAGGGGAGTTGTTATACCTTCGAATC
 Bpu10I
 DdeI
 CviJI
 SfaNI
 DdeI
 CviJI
 AluI
 CviJI
 BceFI
 BsmAI
 CviJI
 HaeIII
 DdeI
 AGAAGCCTTAGCATCAGCCTTAGATAAGGAAGCTCTTGTCTCAACTATATTCTTAGGCCG
 1021 -----+-----+-----+-----+-----+-----+-----+ 1080
 TCTTCGGAATCGTAGTCGGAATCTATTCTTCGAGAACAGAGTTGATATAAGAATCCGGC
 DpnI
 Sau3AI
 BstAPI
 CviRI
 MwoI
 Hpy178III
 AluI
 CviJI
 SspI
 Sth132I
 CjeI
 TGCAAAACTGCCGATCATCTCCTACCTACAAATATTTCATAGCTATCCCGAACATCAAAA
 1081 -----+-----+-----+-----+-----+-----+-----+ 1140
 ACGTTTTTACGGCTAGTAGAGGATGGATGTTTATAAGTATCGATAGGGCTTGTAGTTTT
 AluI
 CviJI
 HindIII
 DraI
 MseI
 BccI
 HindIII
 CjeI
 AluI
 CviJI
 ACAAGAGATGGCACAACGCCAAGCTTACGCTAAAAAACTCTTTAAAGAAGCTTTAGAAGA
 1141 -----+-----+-----+-----+-----+-----+-----+ 1200
 TGTTCTCTACCGTGTTGCGGTTTGAATGCGATTTTTTGAAGAAATTTCTTCGAAATCTTCT
 TaqI
 Hpy178III
 DpnI
 BglIII
 BstYI
 Sau3AI
 TspRI
 BtsI
 MboII
 MseI
 Sth132I
 BscGI
 ACTCCAAATCACTGCTAAAGATCTCGAACATCTTAATCTTATCTTTCCCGTTTCTCTCGTC
 1201 -----+-----+-----+-----+-----+-----+-----+ 1260
 TGAGGTTTGTAGTGACGATTTCTAGAGCTTGTAGAATTAGAATAGAAAGGGCAAAGGAGCAG

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Figure 2 Cont.

```

                                MmeI
                                TspRI |
                                Bst4CI | |
MnlI      BfaI      SpeI | |
|          | |
AGCAAGTTCTTTACTAGTCCAAGTTATACGAGAACAGTGGAAAGAAAGTTTAGGGTTTCGC
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
TCGTTCAAGAAATGATCAGGTTGAATATGCTCTTGTCACCTTTCTTTCAAATCCCAAGCG

                                ApoI
                                MboII
                                Tsp509I
                                Hpy188IX |
                                BslI | |
                                EarI
                                Eco57I
                                SapI MboII      Tth111III
                                | | |
TATCCCTATTGTCGGAAAGGAATTTGCTCTTCTCCAAGCAGACCTATCTTCAGGGAACTT
1321 -----+-----+-----+-----+-----+-----+ 1380
ATAGGGATAACAGCCTTTCTTAAACGAGAAGAGGTTTCGTCTGGATAGAAGTCCCTTGAA

                                DpnI
                                Sau3AI |
                                SfcI
                                AluI |
                                CviJI |
                                MnlI |
                                DrdII
                                BccI | |
                                AlwI
                                BstAPI | |
                                MwoI | |
                                FokI | |
                                DpnI
                                Sau3AI |
CTCTTTAGCTACAGGAGGATGGTTTCGAGACTTTGCTGATCCTATGGCATTCTTAACGAT
1381 -----+-----+-----+-----+-----+-----+ 1440
GAGAAATCGATGTCCTCCTACCAAGCGTCTGAAACGACTAGGATACCGTAAAGATTGCTA

                                CjeI
                                MnlI |
                                CviRI | |
                                Hpy178III
                                BccI | |
                                CjeI
                                ApoI
                                Tsp509I
                                BfaI |
CTTTGCTTATCCATCAGGAGTTCTCCTTATGCAATCAACCATAAGGACTTCTAGAAAT
1441 -----+-----+-----+-----+-----+-----+ 1500
GAAACGAATAGGTAGTCTCAAGGAGGAATACGTTAGTTGGTATTCCTGAAGGATCTTTA

                                DpnI
                                Sau3AI |
                                CjePI | |
                                HphI | | |
                                Tsp509I
                                Hpy188IX |
                                AluI
                                CviJI
                                Cac8I |
                                HindIII |
                                CjePI | |
TCTACAAAACATAGAACAAGAGCAAGATCACCAAAAACGCTCGGAATTAGTGTCGCAAGC
1501 -----+-----+-----+-----+-----+-----+ 1560
AGATGTTTTGTATCTTGTTCTCGTTCTAGTGGTTTTTGCGAGCCTTAATCACAGCGTTCG

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FIG. 2 CONT.

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Figure 2 Cont.

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          BfaI          DpnI
          BsaI |          Sau3AI |
          BsmAI |          CviJI | |
          | |          | | |
TTCTCTTTTACCTAGAGACCTTTCATATTATTGAGCCGATCTACCACGACGCATTTCAATT
1561 -----+-----+-----+-----+-----+-----+-----+ 1620
AAGAGAAATGGATCTCTGGAAAGTATAATAACTCGGCTAGATGGTGCTGCGTAAAGTTAA

          HinfI
          CjeI|
          HphI ||      PleI
          BfaI| ||      BsmAI|
          | | |          | |
TGCTATGAATAAAAAACTTTCTAATCTAGGAGTCTCACCAACAGGAGTTGTGGACTTCCG
1621 -----+-----+-----+-----+-----+-----+-----+ 1680
ACGATACTTATTTTTTGAAGATTAGATCCTCAGAGTGTTGTCCTCAACACCTGAAGGC

          Bpu10I
          DdeI          MnlI          HinfI
          CjeI |Tsp509I      MseI |      Hpy178III      TfiI TaqII
          | |      |          | |          |          | |
TTATGCTAAGGAAAATTAGCACCTCTTTTAATCTCGCAAACCTTGTCAGAAGTGAATCTT
1681 -----+-----+-----+-----+-----+-----+-----+ 1740
AATACGATTCCCTTTTAATCGTGGAGAAAATTAGAGCGTTTGAACAGTTCTTGAAGTTAGAA

          NlaIV          NlaIV
          BsrI|          BanI |
          BanI||          BglI | |
          BmrI |||          MwoI | |
          | |||          | | |
ATACTAAACTGGGTGCCTTTGTGGCACCTCGTTTCTCTGACTGCTCTTCTCTCTCTA
1741 -----+-----+-----+-----+-----+-----+-----+ 1799
TATGATTTGACCCACGGAACACCGTGGAGCAAAGGAAGACTGACGAGAAGAGAGAGAT

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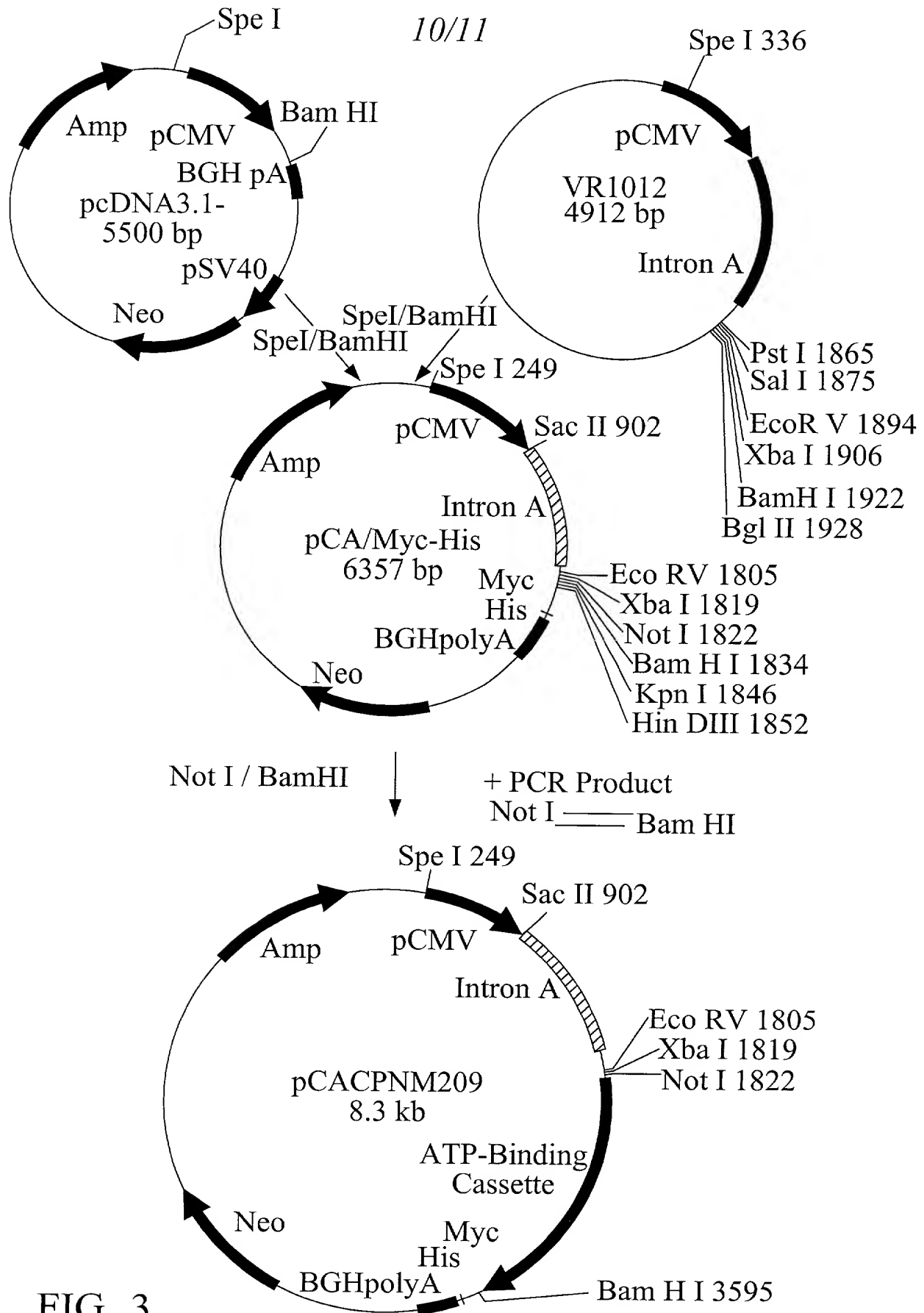


FIG. 3
Construction of pCACPNM209

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Figure 4: Protective efficacy of DNA immunization with pCACPNM209

